

Run on: April 26, 2005, 20:05:04 ; Search time 2.79577 Seconds
 (without alignments)
 8779.016 Million cell updates/sec

OM nucleic - nucleic search, using bw model

Title: US-10-750-976-38
 Perfect score: 15
 Sequence: 1 csgaacccaggaga 15

Scoring table: IDENTITY_NUC
 GapP 10.0 , GapExt 1.0

Searched: 1202784 seqb, 818138359 residues

Total number of hits satisfying chosen parameters: 2405568

Minimum DB seq length: 0
 Maximum DB seq length: 200000000
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued Patents NA:*

1: /cgn2_6/podata/1/ina/5A_COMB.seq: *
 2: /cgn2_6/podata/1/ina/5B_COMB.seq: *
 3: /cgn2_6/podata/1/ina/6A_COMB.seq: *
 4: /cgn2_6/podata/1/ina/6B_COMB.seq: *
 5: /cgn2_6/podata/1/ina/PCITS_COMB.seq: *
 6: /cgn2_6/podata/1/ina/backfileseq.seq: *

Pred. No. 18 is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	15	100.0	15	US-09-204-117B-5
2	14	93.3	1296	Sequence 5, Appli
3	14	93.3	1353	Sequence 1473, Ap
4	14	93.3	3017	Sequence 1974, Ap
5	14	93.3	3233	Sequence 4422, AP
6	14	93.3	4185	Sequence 3585, AP
7	13	89.3	601	Sequence 3646, AP
8	13	89.3	1884	Sequence 157337, AP
9	13	89.3	11382	Sequence 567, AP
10	13	89.3	79756	Sequence 904, AP
11	13	89.3	191433	Sequence 17337, A
12	13	86.7	601	Sequence 6144, A
13	13	86.7	601	Sequence 132415, A
14	13	86.7	601	Sequence 161664, A
15	13	86.7	8264	Sequence 203414, A
16	13	86.7	54531	Sequence 15457, A
17	13	86.7	67962	Sequence 16267, A
18	13	86.7	325791	Sequence 1782, A
19	13	86.7	450395	Sequence 1, Appli
20	13	86.7	670689	Sequence 15453, A
21	13	86.7	670690	Sequence 1205, A
22	13	86.7	440375	Sequence 14207, A
23	13	86.7	4411529	Sequence 2, Appli
24	12	82.7	25	Sequence 1, Appli
25	12	82.7	25	SEQ ID NO: 1473
26	12	82.7	25	LENGTH: 1296
27	12	82.7	25	TYPE: DNA
				ORGANISM: Artificial Sequence
				FEATURE: 428, APP

ALIGNMENTS

RESULT 1	US-09-204-117B-5
Query Match	100.0%; Score 15; DB 3; Length 15;
Best Local Similarity	100.0%; Pred. No. 12;
Matches	15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 CTGAACTCTAGGGGA 15
Db	1 CTGAACTCTAGGGGA 15
LENGTH: 15	
OTHER INFORMATION: mutated Shiga toxin segment	
US-09-204-117B-5	
Query Match	100.0%; Score 15; DB 3; Length 15;
Best Local Similarity	100.0%; Pred. No. 12;
Matches	15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 CTGAACTCTAGGGGA 15
Db	1 CTGAACTCTAGGGGA 15
LENGTH: 15	
OTHER INFORMATION: mutated Shiga toxin segment	
RESULT 2	US-09-710-279-1473
Query Match	100.0%; Score 15; DB 3; Length 15;
Best Local Similarity	100.0%; Pred. No. 12;
Matches	15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 CTGAACTCTAGGGGA 15
Db	1 CTGAACTCTAGGGGA 15
LENGTH: 15	
OTHER INFORMATION: mutated Shiga toxin segment	
RESULT 3	US-09-710-279-1473
Query Match	100.0%; Score 15; DB 3; Length 15;
Best Local Similarity	100.0%; Pred. No. 12;
Matches	15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 CTGAACTCTAGGGGA 15
Db	1 CTGAACTCTAGGGGA 15
LENGTH: 15	
OTHER INFORMATION: mutated Shiga toxin segment	
RESULT 4	US-09-710-279-1473
Query Match	100.0%; Score 15; DB 3; Length 15;
Best Local Similarity	100.0%; Pred. No. 12;
Matches	15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 CTGAACTCTAGGGGA 15
Db	1 CTGAACTCTAGGGGA 15
LENGTH: 15	
OTHER INFORMATION: mutated Shiga toxin segment	
RESULT 5	US-09-710-279-1473
Query Match	100.0%; Score 15; DB 3; Length 15;
Best Local Similarity	100.0%; Pred. No. 12;
Matches	15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 CTGAACTCTAGGGGA 15
Db	1 CTGAACTCTAGGGGA 15
LENGTH: 15	
OTHER INFORMATION: mutated Shiga toxin segment	
RESULT 6	US-09-710-279-1473
Query Match	100.0%; Score 15; DB 3; Length 15;
Best Local Similarity	100.0%; Pred. No. 12;
Matches	15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 CTGAACTCTAGGGGA 15
Db	1 CTGAACTCTAGGGGA 15
LENGTH: 15	
OTHER INFORMATION: mutated Shiga toxin segment	
RESULT 7	US-09-710-279-1473
Query Match	100.0%; Score 15; DB 3; Length 15;
Best Local Similarity	100.0%; Pred. No. 12;
Matches	15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 CTGAACTCTAGGGGA 15
Db	1 CTGAACTCTAGGGGA 15
LENGTH: 15	
OTHER INFORMATION: mutated Shiga toxin segment	
RESULT 8	US-09-710-279-1473
Query Match	100.0%; Score 15; DB 3; Length 15;
Best Local Similarity	100.0%; Pred. No. 12;
Matches	15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 CTGAACTCTAGGGGA 15
Db	1 CTGAACTCTAGGGGA 15
LENGTH: 15	
OTHER INFORMATION: mutated Shiga toxin segment	
RESULT 9	US-09-710-279-1473
Query Match	100.0%; Score 15; DB 3; Length 15;
Best Local Similarity	100.0%; Pred. No. 12;
Matches	15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 CTGAACTCTAGGGGA 15
Db	1 CTGAACTCTAGGGGA 15
LENGTH: 15	
OTHER INFORMATION: mutated Shiga toxin segment	
RESULT 10	US-09-710-279-1473
Query Match	100.0%; Score 15; DB 3; Length 15;
Best Local Similarity	100.0%; Pred. No. 12;
Matches	15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 CTGAACTCTAGGGGA 15
Db	1 CTGAACTCTAGGGGA 15
LENGTH: 15	
OTHER INFORMATION: mutated Shiga toxin segment	
RESULT 11	US-09-710-279-1473
Query Match	100.0%; Score 15; DB 3; Length 15;
Best Local Similarity	100.0%; Pred. No. 12;
Matches	15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 CTGAACTCTAGGGGA 15
Db	1 CTGAACTCTAGGGGA 15
LENGTH: 15	
OTHER INFORMATION: mutated Shiga toxin segment	
RESULT 12	US-09-710-279-1473
Query Match	100.0%; Score 15; DB 3; Length 15;
Best Local Similarity	100.0%; Pred. No. 12;
Matches	15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 CTGAACTCTAGGGGA 15
Db	1 CTGAACTCTAGGGGA 15
LENGTH: 15	
OTHER INFORMATION: mutated Shiga toxin segment	
RESULT 13	US-09-710-279-1473
Query Match	100.0%; Score 15; DB 3; Length 15;
Best Local Similarity	100.0%; Pred. No. 12;
Matches	15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 CTGAACTCTAGGGGA 15
Db	1 CTGAACTCTAGGGGA 15
LENGTH: 15	
OTHER INFORMATION: mutated Shiga toxin segment	
RESULT 14	US-09-710-279-1473
Query Match	100.0%; Score 15; DB 3; Length 15;
Best Local Similarity	100.0%; Pred. No. 12;
Matches	15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 CTGAACTCTAGGGGA 15
Db	1 CTGAACTCTAGGGGA 15
LENGTH: 15	
OTHER INFORMATION: mutated Shiga toxin segment	
RESULT 15	US-09-710-279-1473
Query Match	100.0%; Score 15; DB 3; Length 15;
Best Local Similarity	100.0%; Pred. No. 12;
Matches	15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 CTGAACTCTAGGGGA 15
Db	1 CTGAACTCTAGGGGA 15
LENGTH: 15	
OTHER INFORMATION: mutated Shiga toxin segment	
RESULT 16	US-09-710-279-1473
Query Match	100.0%; Score 15; DB 3; Length 15;
Best Local Similarity	100.0%; Pred. No. 12;
Matches	15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 CTGAACTCTAGGGGA 15
Db	1 CTGAACTCTAGGGGA 15
LENGTH: 15	
OTHER INFORMATION: mutated Shiga toxin segment	
RESULT 17	US-09-710-279-1473
Query Match	100.0%; Score 15; DB 3; Length 15;
Best Local Similarity	100.0%; Pred. No. 12;
Matches	15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 CTGAACTCTAGGGGA 15
Db	1 CTGAACTCTAGGGGA 15
LENGTH: 15	
OTHER INFORMATION: mutated Shiga toxin segment	
RESULT 18	US-09-710-279-1473
Query Match	100.0%; Score 15; DB 3; Length 15;
Best Local Similarity	100.0%; Pred. No. 12;
Matches	15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 CTGAACTCTAGGGGA 15
Db	1 CTGAACTCTAGGGGA 15
LENGTH: 15	
OTHER INFORMATION: mutated Shiga toxin segment	
RESULT 19	US-09-710-279-1473
Query Match	100.0%; Score 15; DB 3; Length 15;
Best Local Similarity	100.0%; Pred. No. 12;
Matches	15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 CTGAACTCTAGGGGA 15
Db	1 CTGAACTCTAGGGGA 15
LENGTH: 15	
OTHER INFORMATION: mutated Shiga toxin segment	
RESULT 20	US-09-710-279-1473
Query Match	100.0%; Score 15; DB 3; Length 15;
Best Local Similarity	100.0%; Pred. No. 12;
Matches	15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 CTGAACTCTAGGGGA 15
Db	1 CTGAACTCTAGGGGA 15
LENGTH: 15	
OTHER INFORMATION: mutated Shiga toxin segment	
RESULT 21	US-09-710-279-1473
Query Match	100.0%; Score 15; DB 3; Length 15;
Best Local Similarity	100.0%; Pred. No. 12;
Matches	15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 CTGAACTCTAGGGGA 15
Db	1 CTGAACTCTAGGGGA 15
LENGTH: 15	
OTHER INFORMATION: mutated Shiga toxin segment	
RESULT 22	US-09-710-279-1473
Query Match	100.0%; Score 15; DB 3; Length 15;
Best Local Similarity	100.0%; Pred. No. 12;
Matches	15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 CTGAACTCTAGGGGA 15
Db	1 CTGAACTCTAGGGGA 15
LENGTH: 15	
OTHER INFORMATION: mutated Shiga toxin segment	
RESULT 23	US-09-710-279-1473
Query Match	100.0%; Score 15; DB 3; Length 15;
Best Local Similarity	100.0%; Pred. No. 12;
Matches	15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 CTGAACTCTAGGGGA 15
Db	1 CTGAACTCTAGGGGA 15
LENGTH: 15	
OTHER INFORMATION: mutated Shiga toxin segment	
RESULT 24	US-09-710-279-1473
Query Match	100.0%; Score 15; DB 3; Length 15;
Best Local Similarity	100.0%; Pred. No. 12;
Matches	15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 CTGAACTCTAGGGGA 15
Db	1 CTGAACTCTAGGGGA 15
LENGTH: 15	
OTHER INFORMATION: mutated Shiga toxin segment	
RESULT 25	US-09-710-279-1473
Query Match	100.0%; Score 15; DB 3; Length 15;
Best Local Similarity	100.0%; Pred. No. 12;
Matches	15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 CTGAACTCTAGGGGA 15
Db	1 CTGAACTCTAGGGGA 15
LENGTH: 15	
OTHER INFORMATION: mutated Shiga toxin segment	
RESULT 26	US-09-710-279-1473
Query Match	100.0%; Score 15; DB 3; Length 15;
Best Local Similarity	100.0%; Pred. No. 12;
Matches	15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 CTGAACTCTAGGGGA 15
Db	1 CTGAACTCTAGGGGA 15
LENGTH: 15	
OTHER INFORMATION: mutated Shiga toxin segment	
RESULT 27	US-09-710-279-1473
Query Match	100.0%; Score 15; DB 3; Length 15;
Best Local Similarity	100.0%; Pred. No. 12;
Matches	15; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
QY	1 CTGAACTCTAGGGGA 15
Db	1 CTGAACTCTAGGGGA 15
LENGTH: 15	
OTHER INFORMATION: mutated Shiga toxin segment	

copyright (c) 1993 - 2005 Compugen Ltd.	GenCore version 5.1.6
OM nucleic - nucleic search, using bw model	
Run on: April 25, 2005, 18:04:09 ; search time 69.3063 seconds	(without alignments) 10487.183 Million cell updates/sec
Title: US-10-750-976-37	
Perfect score: 15	
Sequence: 1 acagcagacgctta 15	
Scoring table: IDENTITY_NUC	
Gapop 10.0 , Gapext 1.0	
Searched: 4708233 seqs, 24227607955 residues	
Total number of hits satisfying chosen parameters: 9416466	
Minimum DB seq length: 0	
Maximum DB seq length: 2000000000	
Post-processing: Minimum Match 0%	
Maximum Match 100%	
Listing first 45 summaries	
Database : GenBank:*	
1: gb_ba:*	
2: gb_btg:*	
3: gb_ln:*	
4: gb_on:*	
5: gb_ov:*	
6: gb_pat:*	
7: gb_ph:*	
8: gb_pl:*	
9: gb_pr:*	
10: gb_ro:*	
11: gb_stb:*	
12: gb_sy:*	
13: gb_un:*	
14: gb_vl:*	
Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.	
SUMMARIES	
Result No. Score Query Match Length DB ID	Description
1 15 100.0 3959 14 AY547458	RESULT 1
2 15 100.0 21113 2 CR391962	AY47458
3 14 93.3 714 9 HSA327219	LOCUS
4 14 93.3 3312 3 AY433803	DEFINITION
5 14 93.3 5069 5 AY398560	3959 bp RNA
6 14 93.3 10221 1 AE014558	lineair
7 14 93.3 10495 1 AR009700	VRL 04-AUG-2004
8 9 93.3 24523 1 AE008756	AC391962 Dani orner
9 14 93.3 36748 7 AY559836	AU277219 Homo Sapi
10 14 93.3 39949 3 AC009782	AY333803 Trypanoso
11 14 93.3 106255 3 AC108135	AE039856 Galu ga
12 14 93.3 110000 2 AP066498_7	AE014558 Brucella
13 14 93.3 133713 3 AC087838	AE009700 Brucella
14 14 93.3 147226 9 AC013602	AE008756 Salmonell
15 14 93.3 152770 9 AC026005	AY339836 Burkholde
16 14 93.3 173839 9 AC182005	AC009782 Leishmanni
17 14 93.3 181097 2 AC118205	AC108135 Leishmanni
18 14 93.3 217285 2 AC126317	Continuation (8 of
19 14 93.3 233050 1 AL627271	AC087838 Leishmanni
C 20 14 93.3 260760 2 AC127861	AC127861 Rattus no
C 21 14 93.3 295050 1 AL591982	AL591982 Listeria
C 22 14 93.3 30523 1 AE016838	AE016838 Salmonell
C 23 14 93.3 311600 1 AE016755	AE016755 Escherich
C 24 14 93.3 340750 1 BX224135	AE016871 Pseudomon
C 25 14 93.3 349980 5 AX641671	BX294135 Pirellula
C 26 14 93.3 155 8 HV19R	AE641671 Sequence
C 27 13.4 89.3 227 8 HVEL323LR	284539 H. vulgare B
C 28 13.4 89.3 231 8 HVEL329TR	284559 H. vulgare B
C 29 13.4 89.3 232 8 HVEL324NR	284560 H. vulgare B
C 30 13.4 89.3 243 6 AR321328	AR321328 Sequence
C 31 13.4 89.3 318 6 AX048488	AX048488 Sequence
C 32 13.4 89.3 318 6 AX048489	AX048489 Sequence
C 33 13.4 89.3 356 6 HV08492R	284554 H. vulgare B
C 34 13.4 89.3 413 6 CO491384	CQ491384 Sequence
C 35 13.4 89.3 640 14 AFR22856	AFR22856 Caprine a
C 36 13.4 89.3 798 6 AR388811	AR388811 Sequence
C 37 13.4 89.3 817 8 PSU58023	US502 Pseudoeleg
C 38 13.4 89.3 858 11 CNS0613J3B	AL401085 T7 end of
C 39 13.4 89.3 1074 6 AR386650	AR386650 Sequence
C 40 13.4 89.3 1104 8 AB189674	AB189674 Phleodend
C 41 13.4 89.3 1238 1 AB14823	AB174823 Cellulomo
C 42 13.4 89.3 1281 9 BC064028	BC064028 Homo Sapi
C 43 13.4 89.3 1404 3 AFR26516	AFR26516 Puniculin
C 44 13.4 89.3 1539 6 AX568254	AX568254 Sequence
	ALIGNMENTS
	RESULTS
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OM nucleic - nucleic search, using SW model
Run on: April 26, 2005, 16:32:44 ; Search time 20.7192 Seconds
(without alignments)
9714.213 Million cell updates/sec

Title: US-10-750-976-36
Perfect score: 34
Sequence: 1 agatcnncaanatccacagggatatctatgtg 34

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 1.0

Searched: 4390206 sqs, 295987067 residues

Total number of hits satisfying chosen parameters: 8780412

Minimum DB seq length: 0
Maximum DB seq length: 200000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database :

1: geneseqn1980b:*

2: geneseqn1990b:*

3: geneseqn2000b:*

4: geneseqn2001ab:*

5: geneseqn2001bs:*

6: geneseqn2002ab:*

7: geneseqn2002bs:*

8: geneseqn2003ab:*

9: geneseqn2003bs:*

10: geneseqn2003cb:*

11: geneseqn2003ds:*

12: geneseqn2004ab:*

13: geneseqn2004bs:*

Result

Result No.	Score	Query Match Length	DB ID	Description
1	25	76.5	33	3 AAA07572
2	26	76.5	4196	3 ADA30825
3	23	67.6	32	3 AAA07557
4	22.8	67.6	32	3 AAA08039
5	22.2	65.3	349	5 ABV09570
6	22.2	65.3	400	5 ABV30746
7	22.2	65.3	400	5 ABV3714
8	21.2	62.4	33	2 AAQ24139
9	21.2	62.4	3712	2 AAQ97490
10	21.2	62.4	3754	2 AAQ57800
11	21.2	62.4	3754	2 AAQ85420
12	21.2	62.4	3769	2 AAQ57811
13	21.2	62.4	3769	2 AAQ97492
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15	21.2	62.4	4377	2 AAQ85421
16	20.6	60.2	700	2 AAH9629
17	19.8	58.2	77287	9 AAD58251
18	19.8	58.2	82938	6 ABV72623
19	19.8	58.2	110000	13 ABV3229_1
20	19.8	58.2	167739	9 AAD58258

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

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OM nucleic - nucleic search, using sw model
Run on: April 26, 2005, 11:14:05 ; Search time 83.643 Seconds
(without alignments)

8689.645 Million cell updates/sec
Title: US-10-750-965-39
Perfect score: 15
Sequence: 1 gaattgcgcagg 15

Scoring table: IDENTITY NUC
Gapov 10.0 , Gapext 1.0
Searched: 4108233 seqs, 24227607955 residues

Total number of hits satisfying chosen parameters: 9416466
Minimum DB seq length: 0
Maximum DB seq length: 200000000
Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : GenBank:
1: gb:ba: *
2: gb:hg: *
3: gb:in: *
4: gb:om: *
5: gb:ov: *
6: gb:pat: *
7: gb:ph: *
8: gb:pl: *
9: gb:pr: *
10: gb:ro: *
11: gb:stb: *
12: gb:by: *
13: gb:un: *
14: gb:vi: *

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SUMMARIES

Result No.	Score	Query Match Length	DB ID	Description
1	15	100.0	1924	9 AK129669
2	100.0	3137	8 NC_0243517	
3	100.0	35666	9 BX119906	
4	100.0	197666	2 AC138145	
5	100.0	19017	9 AC100832	
6	100.0	349841	1 BX572606	
7	14	93.3	385 6 CQ472848	
8	93.3	396 6 CQ478754		
9	93.3	417 6 CQ49586		
10	93.3	428 6 CQ420217		
11	93.3	430 6 CQ503156		
12	93.3	438 6 CQ49951		
13	93.3	438 6 CQ508919		
14	93.3	438 6 CQ512005		
15	93.3	459 6 CQ592166		
16	93.3	559 6 BD152296		
17	93.3	559 6 AX872234		
18	93.3	594 6 CQ489052		
19	93.3	594 6 CQ491123		

ALIGNMENTS

RESULT 1
AK129669
LOCUS AK129669 1924 bp mRNA linear PRI 10-SEP-2003
DEFINITION Homo sapiens cDNA FLJ26158 Fis, clone ADG01579.
ACCESSION AK129669
VERSION AK129669.1 GI:34524262
KEYWORDS oligo capping; fis (full insert sequence).
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominoidea; Homo.
REFERENCE 1 Tashiro,H., Yamazaki,M., Watanabe,K., Kumagai,A., Itakura,S., Fukushima,Y., Fujimoto,Y., Komiyama,M., Suzuki,Y., Hata,H., Nakagawa,K., Mizuno,S., Morinaga,M., Kawamura,M., Sugiyama,T., Irie,R., Otsuki,T., Sato,H., Nishikawa,T., Sugiyama,A., Kawakami,B., Nagai,K., Isogai,T. and Sugano,S.
TITLE NEDO human cDNA sequencing project
JOURNAL Unpublished
REFERENCE 2 Sugano,S. and Suzuki,Y.
AUTHORS Sugano,S. and Suzuki,Y.
TITLE Direct Submission
JOURNAL Submitted (31-DEC-2003) Sumio Sugano, Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center, Shirokane-tai, 4-6-1, Minato-ku, Tokyo 108-8639, Japan
(E-mail: flicdn@ims.u-tokyo.ac.jp, Tel: 81-3-5449-5286, Fax: 81-3-5449-5416)
COMMENT NEDO human cDNA sequencing project supported by Ministry of Economy, Trade and Industry of Japan; cDNA full insert sequencing; Research Association for Biotechnology (RAB); cDNA library construction and 5'-end one pass sequencing; Institute of Medical Science, University of Tokyo, Laboratory of Genome Structure, Human Genome Center, 3, and one pass sequencing; RAB; clone Selection for full insert sequencing; RAB and Helix Research Institute.
FEATURES Location/Qualifiers 1. 1924
/organism="Homo sapiens"
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/clone="ADG01579"
/tissue_type="adrenal gland"
/clone_lib="ADG"

